


(TM)

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WPrsch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Aug 6 14:08:28 1998; MasPar time 13.37 Seconds
Tabular output not generated. 765.547 Million cell updates/sec

Title: >US-08-813-323A-1
Description: (324-566) from US08813323A.pep (3 of 3)
Perfect Score: 1764
Sequence: 1 SQAELKELDKREIRFRQNW.....YIKDDTIFIKVIVDTSDLPD 243

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 45.863; Variance 93.351; scale 0.491

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1764	100.0	567	10	TNF RECEPTOR-ASSOCIATE	0.00e+00
2	1758	99.7	567	10	TNF RECEPTOR-ASSOCIATE	0.00e+00
3	1754	99.4	568	2	LMP1 ASSOCIATED PROTEIN	0.00e+00
4	1754	99.4	568	2	CD40 RECEPTOR ASSOCIAT	0.00e+00
5	1747	99.0	543	2	CD40-ASSOCIATED PROTEIN	0.00e+00
6	1740	98.5	567	2	CD40 BINDING PROTEIN	0.00e+00
7	909	51.5	558	10	TNF RECEPTOR-ASSOCIATE	7.18e-153
8	908	51.5	558	10	TNF RECEPTOR-ASSOCIATE	1.15e-152
9	894	50.7	538	2	TNF RECEPTOR ASSOCIATE	7.96e-150
10	730	41.4	416	2	EPSTEIN-BARR VIRUS-IND	1.01e-116
11	663	37.6	501	2	TUMOR NECROSIS FACTOR	2.52e-103
12	437	24.8	470	2	CYSTINE RICH DOMAIN AS	5.51e-59
13	407	23.1	470	10	CYSTINE RICH MOTIF AS	3.02e-53
14	337	19.1	530	10	TNF RECEPTOR-ASSOCIATE	4.59e-40
15	117	6.6	284	3	TROPOMYOSIN	7.04e-03
16	117	6.6	284	3	TROPOMYOSIN	7.04e-03
17	117	6.6	299	3	MAG44 (FRAGMENT)	7.04e-03
18	114	6.5	284	12	FAST MUSCLE TROPOMYOSI	1.78e-02
19	113	6.4	248	10	ALPHA-TROPOMYOSIN 5A	2.42e-02
20	113	6.4	248	10	ALPHA-TROPOMYOSIN 5B	2.42e-02

21	113	6.4	535	9	P72839	HYPOTHETICAL 61.7 KD P	2.42e-02
22	113	6.4	4096	2	Q13327	DNA DEPENDENT PROTEIN	2.42e-02
23	113	6.4	4127	2	P78527	DNA-DEPENDENT PROTEIN	2.42e-02
24	111	6.3	847	2	Q16584	PROTEIN KINASE	4.45e-02
25	111	6.3	1060	10	Q62036	5-AZACYTIDINE INDUCED	4.45e-02
26	110	6.2	284	3	Q25145	TROPOMYOSIN	6.02e-02
27	110	6.2	538	3	Q25616	CIRCULATING ANTIGEN	6.02e-02
28	109	6.2	772	3	Q23529	SIMILAR TO PARAMYOSIN	8.13e-02
29	107	6.1	204	10	P70525	RAT STRIATED MUSCLE AL	1.47e-01
30	107	6.1	243	2	Q15657	TROPOMYOSIN ISOFORM	1.47e-01
31	107	6.1	280	10	P70524	RAT SMOOTH MUSCLE ALPH	1.47e-01
32	107	6.1	284	12	Q91490	SLOW MUSCLE TROPOMYOSI	1.47e-01
33	107	6.1	284	12	Q90348	CARDIAC TROPOMYOSIN	1.47e-01
34	107	6.1	284	10	Q63582	NON-MUSCLE ALPHA TROPO	1.47e-01
35	107	6.1	284	10	Q63607	ALPHA-TROPOMYOSIN 3	1.47e-01
36	107	6.1	284	10	Q63583	HEPATOMA ALPHA TROPOMY	1.47e-01
37	107	6.1	338	2	O00377	L1 ELEMENT L1.39 P40 A	1.47e-01
38	107	6.1	338	2	O00374	L1 ELEMENT L1.25 P40 A	1.47e-01
39	107	6.1	981	8	O04612	A-IG002N01.24	1.47e-01
40	108	6.1	1410	3	Q20439	T18P3.4 (FRAGMENT)	1.10e-01
41	106	6.0	337	2	O00373	L1 ELEMENT L1.24 P40	1.98e-01
42	106	6.0	510	3	Q24425	TROPOMYOSIN GENE ISOFO	1.98e-01
43	106	6.0	633	3	Q17048	CYTOPLASMIC INTERMEDIA	1.98e-01
44	106	6.0	2648	3	O18291	ZK1151.2	1.98e-01
45	106	6.0	3187	10	Q63714	RAT GCP360	1.98e-01

ALIGNMENTS

RESULT 1
ID Q60803 PRELIMINARY; PRT; 567 AA.
AC Q60803;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE TNF RECEPTOR-ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1).
GN TRAF3 OR CRAFT.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA CHENG G., CLEARY A.M., YE Z., HONG D.I., LEDERMAN S., BALTIMORE D.;
RL SUBMITTED (APR-1995) TO ENBL/GENBANK/DBJ DATA BANKS.
CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; U21050; G719293; -.
DR MGD; MGI:108041; TRAF3.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
KW ZINC-FINGER.
SQ SEQUENCE 567 AA; 64263 MW; F85A30F3 CRC32;

Query Match	100.0%	Score	1764	DB	10	Length	567
Best Local Similarity	100.0%	Pred. No.	0.00e+00				
Matches	243	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Db	324	SOAEKLELDKREIRFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ	383				
Qy	324	SOAEKLELDKREIRFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ	383				
Db	384	LSRHDQTLVSHDIRLADMDLRFQVLETASYNGVLWIKIRYKRRKQBAVMGKTLISLSQ	443				
Qy	384	LSRHDQTLVSHDIRLADMDLRFQVLETASYNGVLWIKIRYKRRKQBAVMGKTLISLSQ	443				
Db	444	FYTGFGKMCARYLNGDGMKGKTHLSLFFVIMRGYDALLPFPFKQKVTLMMDGSS	503				
Qy	444	FYTGFGKMCARYLNGDGMKGKTHLSLFFVIMRGYDALLPFPFKQKVTLMMDGSS	503				
Db	504	RRHLDGAFKPDPSNSSFKKPTGEMNIASGCPVFAQVLENGTVIKDDTIFIKVIVDTSD	563				
Qy	504	RRHLDGAFKPDPSNSSFKKPTGEMNIASGCPVFAQVLENGTVIKDDTIFIKVIVDTSD	563				
Db	564	LPD 566					

QY 564 LPD 566

RESULT 2

ID Q62380 PRELIMINARY; PRT; 567 AA.
AC Q62380;
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE TNF RECEPTOR-ASSOCIATED FACTOR 3 (TRAFAMN).
GN TRAF3 OR TRAFAMN.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-BRAIN;
RA WANG X., BORNISLAAGER E., HAUB O., TOMIHARA-NEUBERGER C.,
RA LONBERG N., DINULOS M.B., DISTECHE C.M., COPELAND N.,
RA GILBERT D.J., JENKINS N.A., LACY E.,
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U33840; G1488198;
DR MGD; MGI:108041; TRAF3.
SQ SEQUENCE 567 AA; 64376 MW; 7F4F873B CRC32;

Query Match 99.7%; Score 1758; DB 10; Length 567;
Best Local Similarity 99.6%; Pred. No. 0.00e+00;
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 324 SQAEKLKELDKKEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 383
QY 324 SQAEKLKELDKKEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 383
Db 384 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 443
QY 384 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 443
Db 444 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMLMDQSS 503
QY 444 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMLMDQSS 503
Db 504 RRLHGAFAKPDNPSSFFKPTGEMNIASGCPVFAQTVLNGTYIKDDTIFIKVIVDTSD 563
QY 504 RRLHGAFAKPDNPSSFFKPTGEMNIASGCPVFAQTVLNGTYIKDDTIFIKVIVDTSD 563
Db 564 LPD 566
QY 564 LPD 566

RESULT 3 PRELIMINARY; PRT; 568 AA.

ID Q13076
AC Q13076;
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE LMP1 ASSOCIATED PROTEIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOID TUMOR;
RA MEDLINE; 95163092.
RA MOSTALOS G., BIRKENBACH M., YALAMANCHILI R., VANARSDALE T., WARE C.,
RA KIEFF E.;
RL CELL 80:389-399(1995).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; U19260; G675460;
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
KW ZINC-FINGER.
SQ SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;

Query Match 99.4%; Score 1754; DB 2; Length 568;
Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SQAEKLKELDKKEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 384
QY 325 SQAEKLKELDKKEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 384
Db 385 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 444
QY 385 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 444
Db 445 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMLMDQSS 504
QY 445 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMLMDQSS 504
Db 505 RRLHGAFAKPDNPSSFFKPTGEMNIASGCPVFAQTVLNGTYIKDDTIFIKVIVDTSD 564
QY 505 RRLHGAFAKPDNPSSFFKPTGEMNIASGCPVFAQTVLNGTYIKDDTIFIKVIVDTSD 564
Db 565 LPD 567
QY 565 LPD 567

RESULT 4 PRELIMINARY; PRT; 568 AA.

ID Q13114
AC Q13114;
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE CD40 RECEPTOR ASSOCIATED FACTOR 1.
GN CRAFT.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95184010.
RA CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D.;
RL SCIENCE 267:1494-1498(1995).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; U21092; G726088;
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
KW ZINC-FINGER.
SQ SEQUENCE 568 AA; 64460 MW; 77A8CDB8 CRC32;

Query Match 99.4%; Score 1754; DB 2; Length 568;
Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SQAEKLKELDKKEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 384
QY 325 SQAEKLKELDKKEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 384
Db 385 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 444
QY 385 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 444
Db 445 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMLMDQSS 504
QY 445 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMLMDQSS 504
Db 505 RRLHGAFAKPDNPSSFFKPTGEMNIASGCPVFAQTVLNGTYIKDDTIFIKVIVDTSD 564
QY 505 RRLHGAFAKPDNPSSFFKPTGEMNIASGCPVFAQTVLNGTYIKDDTIFIKVIVDTSD 564
Db 565 LPD 567
QY 565 LPD 567

RESULT 5

ID	Q13947	PRELIMINARY;	PRT;	543 AA.
AC	Q13947;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DT	CD40-ASSOCIATED PROTEIN.			
GN	CAP-1.			
DE	HOMO SAPIENS (HUMAN).			
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
OC	[1]			
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RC	MEDLINE; 95129692.			
RX	SATO T., IRIE S., REED J.C.;			
RA	FEBS LETT. 358:113-118(1995).			
RL	-I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.			
RL	EMBL; L38509; G695358; -			
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.			
DR	ZINC-FINGER.			
KW	SEQUENCE 543 AA; 61719 MW; E9FCA764 CRC32;			
SQ				
Query Match				
Best Local Similarity 98.0%; Score 1747; DB 2; Length 543;				
Matches 240; Conservative 1; Mismatches 2; Indels 0; Gaps 0;				
Db	300	SQAEKLEKELDKETRSPQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNLTGLESQ	359	
QY	324	SQAEKLEKELDKETRSPQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNLTGLESQ	383	
Db	360	LSRHDQMLSVHDIRLADMDLRFQVLETSYNGVLIWKIRDYKRRKQEAVMGKTLISYQ	419	
QY	384	LSRHDQMLSVHDIRLADMDLRFQVLETSYNGVLIWKIRDYKRRKQEAVMGKTLISYQ	443	
Db	420	FYTGEGYKMCARVYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQVTLMLMDQGS	479	
QY	444	FYTGEGYKMCARVYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQVTLMLMDQGS	503	
Db	480	RHGLDAFPDNPSSSKFKPTGEMNTASGCPVFVAQTVLENGTYIKDDTIFIKVIIVDTSD	539	
QY	504	RHGLDAFPDNPSSSKFKPTGEMNTASGCPVFVAQTVLENGTYIKDDTIFIKVIIVDTSD	563	
Db	540	LPD 542		
QY	564	LPD 566		
RESULT 6				
ID	Q12990	PRELIMINARY;	PRT;	567 AA.
AC	Q12990;			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DT	CD40 BINDING PROTEIN.			
GN	CD40BP.			
DE	HOMO SAPIENS (HUMAN).			
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
OC	[1]			
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE; 95073988.			
RX	HU H.M., O'ROURKE K., BOGUSKI M.S., DIXIT V.M.;			
RA	J. BIOL. CHEM. 269:30069-30072(1994)			
RL	-I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.			
RL	EMBL; U15637; G595911; -			
CC	PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.			
DR	ZINC-FINGER.			
DR	SEQUENCE 567 AA; 64277 MW; 441E3FC6 CRC32;			
KW				
SQ				
Query Match				
Best Local Similarity 98.6%; Score 1740; DB 2; Length 567;				
Matches 240; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE TNF RECEPTOR-ASSOCIATED FACTOR 5 (TRAF5).
 GN TRAF5.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE; 96278943.
 RA NAKANO H., OSHIMA H., CHUNG W., WILLIAMS-ABBOTT L., WARE C.F.,
 RA YAGITA H., OKUMURA K.,
 RL J. BIOL. CHEM. 271:14661-14664(1996).
 CC -I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 DR EMBL; D78141; G1469893; -.
 DR MGI; G107548; TRAF5.
 DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
 KW ZINC-FINGER.
 SQ SEQUENCE 558 AA; 64154 MW; 910ACC60 CRC32;
 Query Match 51.5%; Score 908; DB 10; Length 558;
 Best Local Similarity 50.4%; Pred. No. 1.15e-152;
 Matches 124; Conservative 58; Mismatches 59; Indels 5; Gaps 4;
 Db 314 SHTRKSAWLEAQRHLLQI-VNQPSRLDLRLSLVDVSVKQRIQTLEASDORLV-LLEG 371
 QY 324 SQAELKELDKETPRFRQNEEADSMKSVESLQKRVTEL-ESVDKSAGQAARNTGLLES 382
 Db 372 ETSKDHAINIKHAOLNKEERFKLEGACYGKLIWYTDYRVKKRAVEGHTVSFVSQ 431
 QY 383 QLSRHQDTLSVHDRLADMDLRFQVLETASVNGVLIWKIRDYKRRKQAVMGKTLISLSQ 442
 Db 432 PFYTSRCYRLCARAYLNGDGSKGTHLSLYFVVMRGEFDSLLQWFFRQVRVTLMLDQSG 491
 QY 443 PFYTFYGYKMCARVYLNGDGMKGTHLSLYFVVMRGEYDALLPWFPPKQVTLMLDQGS 502
 Db 492 KKHIVETKADPNSSFRPQGMNIASGCPFRVSHSTLNSKTYIKDPTFLFKVAVD 551
 QY 503 SRRLGDAFKDPDNPSSFKKPTGEMNIASGCPVFAQTVLENG--TYIKDDTIFIKVID 560
 Db 552 LTDLDD 557
 QY 561 TSDLPD 566
 RESULT 9
 ID 000463 PRELIMINARY; PRT; 538 AA.
 AC 000463;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE TNF RECEPTOR ASSOCIATED FACTOR 5 (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE; 97321041.
 RA NAKANO H., SHINDO M., YAMADA K., YOSHIDA M.C., SANTEE S.M., WARE C.F.,
 RA JENKINS N.A., GILBERT D.J., YAGITA H., COPELAND N.G., OKUMURA K.,
 RL GENOMICS 42:26-32(1997).
 CC -I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 DR EMBL; U69108; G2138180; -.
 DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
 KW ZINC-FINGER.
 FT NON_TER
 SQ SEQUENCE 538 AA; 62238 MW; 57B3F125 CRC32;
 Query Match 50.7%; Score 894; DB 2; Length 538;
 Best Local Similarity 59.2%; Pred. No. 7.96e-150;
 Matches 113; Conservative 47; Mismatches 28; Indels 3; Gaps 2;

Db 348 AVLEETNKHDTHINIKHAOLSKNEERFKLEGTGCVNGKLIWKVDYKMKREAVDGHTV 407
 QY 378 GLLESLSRHQDTLSVHDRLADMDLRFQVLETASVNGVLIWKIRDYKRRKQAVMGKTL 437
 Db 408 SIFSQSFYTSRCYRLCARAYLNGDGSGRGSHLSLYFVVMRGEFDSLLQWFFRQVRVTLML 467
 QY 438 SLYSQPFYTFYGYKMCARVYLNGDGMKGTHLSLYFVVMRGEYDALLPWFPPKQVTLML 497
 Db 468 LDQ-SGKKNIMETFKPDPPNSSFSFKRDPDGEWNIASGCPREVAHSVLENKAKYIKDDTLFL 526
 QY 498 MDQSGRRRHGLGDAFKPDPPNSSFSFKRDPDGEWNIASGCPVFAQTVLENG--TYIKDDTIFI 555
 Db 527 KVAVDLTDLDD 537
 QY 556 KVIYDTSDLDPD 566
 RESULT 10
 ID Q13077 PRELIMINARY; PRT; 416 AA.
 AC Q13077;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
 DE EPSTEIN-BARR VIRUS-INDUCED PROTEIN.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPHOID TUMOR;
 RA MOSIALOS G., BIRKENBACH M., YALAMANCHILI R., VANARSDALE T., WARE C.,
 RA KIEFF E.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U19261; G673462; -.
 SQ SEQUENCE 416 AA; 46163 MW; 760442BC CRC32;
 Query Match 41.4%; Score 730; DB 2; Length 416;
 Best Local Similarity 51.3%; Pred. No. 1.01e-116;
 Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
 Db 222 SQDDRILSLRORVELQOTLAQDQALGKLEQSLRLMEASFDGTFWKTINTVTRCH 281
 QY 371 GQAARNTGL-LESQLSRHQDTLSVHDRLADMDLRFQVLETASVNGVLIWKIRDYKRRKQ 429
 Db 282 ESACGRVSLSPAFYAKYKYLCLRLYLINGDGTCKRTHLSLYFVIMRGEYDALLPWF 341
 QY 430 EAVMGKTLISQPFYTFYGYKMCARVYLNGDGMKGTHLSLYFVIMRGEYDALLPWF 489
 Db 342 RNKVTFLDQ-NNREHAIDAFRDLSSASFQRPQSETNVASGCPFLFPLSKLQSPKHAY 400
 QY 490 KQKVTMLMDQSGRRRHGLGDAFKPDPPNSSFSFKKPTGEMNIASGCPVFAQTVLENG--TY 547
 Db 401 VKDITMLKIVETS 415
 QY 548 IKDDTIFIKVIDTS 562
 RESULT 11
 ID Q12933 PRELIMINARY; PRT; 501 AA.
 AC Q12933;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3.
 GN TRAF3.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 9536558.
 RA SONG H.Y., DONNER D.B.,
 RL BIOCHEM. J. 309:825-829(1995).

QY	402	DLRFQVLE-TASYNGVLIWKIRDYKRRKQEAVMGKTLISLSYQSPFYTGFGYFKYKMCARVYL	460
Db	354	GNSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFESLLDQSDPLGAKPOHVTETFPDPN	413
QY	461	GDGMKGTHLSLFFVIMRGEVDALLPWFQKVLMMLMDQG--S-SR-RHLGDAFAPDPN	516
Db	414	WNFKQPGTWGSLDDESLGFGPKFTISHQDIRKNRYVRDADFIRAAVE	463
QY	517	SSSFKKP-T-GEMNIAS--GCPVFAQTVLENGTYIKDDTIFIKVIVD	560
RESULT	13		
ID	Q61382	PRELIMINARY; PRT; 470 AA.	
AC	Q61382;		
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)		
DE	CYSTEINE RICH MOTIF ASSOCIATED TO RING AND TRAF DOMAINS PROTEIN		
DE	(MCARTI).		
GN	CART1.		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RA	REGNIER C.H.;		
RC	SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.		
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.		
DR	EMBL: X92346; G1041446; -		
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.		
KW	ZINC-FINGER.		
SQ	SEQUENCE 470 AA; 53418 MW; 42968389 CRC32;		
Query Match	23.1%; Score 407; DB 10; Length 470;		
Best Local Similarity	38.8%; Pred. No. 3 02e-53;		
Matches	66; Conservative 45; Mismatches 48; Indels 11; Gaps		
Db	294 ELRRELEELISGDVLWIKGYSYGRROEAKAKPNLECFSPAFYTHKYGKLQVSASLN	353	
QY	402 DLRFQVLE-TASYNGVLIWKIRDYKRRKQEAVMGKTLISLSYQSPFYTGFGYFKYKMCARVYL	460	
Db	354 GNSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFESLLDQSDPLGAKPOHVTETFPDPN	413	
QY	461 GDGMKGTHLSLFFVIMRGEVDALLPWFQKVLMMLMDQG--S-SR-RHLGDAFAPDPN	516	
Db	414 WNFKQPGTWGSLDDESLGFGPKFTISHQDIRKNRYVRDADFIRASVE	463	
QY	517 SSSFKKP-T-GEMNIAS--GCPVFAQTVLENGTYIKDDTIFIKVIVD	560	
RESULT	14		
ID	P70196	PRELIMINARY; PRT; 530 AA.	
AC	P70196;		
DT	01-FEB-1997 (TREMBLREL. 02, CREATED)		
DT	01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)		
DE	TNF RECEPTOR-ASSOCIATED FACTOR 6 (TRAF6).		
DE	GN		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RA	ISHIDA T., WATZUSHIMA S., AZUMA S., KOBAYASHI N., TOJO T., SUZUKI K.,		
RA	AIZAWA T., MIYANABE T., MOSTALOS G., KIEFF E., YAMAMOTO T., INOUE J.;		
CC	J. BIOL. CHEM. 271:28745-28748(1996)		
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.		
DR	EMBL: D84655; G1651195; -		
DR	MGI:108072; TRAF6.		
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.		
KW	ZINC-FINGER.		
SQ	SEQUENCE 530 AA; 60082 MW; C59CCFEB CRC32;		

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Query Match 19.1%; Score 337; DB 10; Length 530;
 Best Local Similarity 30.5%; Pred. No. 4.59e-40; Indels 9; Gaps 8;
 Matches 64; Conservative 46; Mismatches 91; Indels 9; Gaps 8;

Db 304 EFTIKQLESRLVRQDHQIRELTAKMETQ-SMYVGELK-RTIRTE-D-KVAEMEAOCCNG 359
 QY 357 QNRVTELESVDKSAQAARN-TGLESQRHDQTLSDHDIRLADMDLRFQVLETASYNG 415
 Db 360 IYIWKIGFGMHLKSOEERPVVHSPGFTYGRGKLCMLHLQLPTAORCANYISLFF 419
 QY 416 VLIWKIRDKRKQKQAVAGKTLISQPFYGYGYKMCARVYLNQDGMKG-GTHLSLFF 474
 Db 420 HYMQEYDHLWPFGQITRLTILDOSEALIRQNHVEEVMADKPELLAFORPTIPRNPKEF 479
 QY 475 VIMRGEYDALLPFPFKQKVTMLMDQSS--RRHLGDAFKDPDNNSSFFKKPTGEMNIAS- 531
 Db 480 GYVTFMHLRALRQGTIFIKDDTLVRCVST 509
 QY 532 GCPVFAQTVLENGTIVIKDDTIFIKVIVDT 561

RESULT 15
 ID O16188 PRELIMINARY; PRT: 284 AA.
 AC O16188;
 DT 01-JAN-1998 (TREMBREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)
 DE TROPOMYOSIN.
 OS DERMATOPHAGOIDES PTERONYSSINUS (HOUSE-DUST MITE).
 OC EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ACARI.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SMITH W. MILLS K.L., THOMAS W.R.:
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AF016278; G2353266;
 DR PROSITE; PS00326; TROPOMYOSIN; 1.
 SQ SEQUENCE 284 AA; 32973 MW; E1BAF90B CRC32;

Query Match 6.6%; Score 117; DB 3; Length 284;
 Best Local Similarity 17.3%; Pred. No. 7.04e-03;
 Matches 13; Conservative 26; Mismatches 35; Indels 1; Gaps 1;

Db 41 BEVRALOKKIOQIENELDQVQELSAANTKLEKEKALQTAEGDVAALNRRIOLEEDLE 100
 QY 327 EKLKELDKIIRPFQNWEEA-DSMKSSVESLQNRVTELESVDKSAQAARNYGLLESQLS 385
 Db 101 RSEERLKIATAKLEE 115
 QY 386 RHDQTLSDHDIRLAD 400

Search completed: Thu Aug 6 14:09:57 1998
 Job time : 89 secs.